

FIG. 1**Human NRSF Amino Acid Sequence**

MATQVMGSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAP
 QLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVGDNNFSDSEEGEGLEESADIKGE
 PHGLENMELRSLSESVVEPQPVFEASGAPDIYSSNKDLPETPGAEDKGKSSKTKPFR
 CKPCQYEAEESEEQVHHIRVHSAKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRC
 DRGYNNTNRYDHYTAHLKHHTRAGDNERVYKCICTYTTVSEYHWRKHLRNHFPRKVY
 TCGKCNFYFSDRKNYVQHVTRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFC
 DQCSYVASNQHEVTRHARQVHNGPKPLNCPHC DYKTADRSNFKKHVELHVNPRQFNCP
 VCDYAASKKCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNIITNEKTEIEQ
 TKIKGDVAGKKNEKSVKAEKRDVSKKPKSNNVSVIQVTTRTRKSVTEVKEMDVHTGS
 NSEKFSKTKKSKRKLEVDSHSLHGPVNDEESTK KKKVESKSKNNNSQEVPKGDSKVE
 ENKKQNTCMKKSTKKTLKNKSSKSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKG
 PVQVELPPPMHAQMEGAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAIVL
 AHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAPMQVVQKEPVQMELSPPMEEVV
 QKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPP
 PPREPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVS
 TEDLSPSPPLPKENLREEASGDQKLLNTGEGNKEAPLQVGAEEADESLPGLAANIN
 ESTHISSSGQNLTPEGETLNGKHQTDIVCEMKMDTDQNTRENLTGINSTVEEPVSP
 MLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGHSHSGSDLSDNMSEGSDDS
 GLHGARPVPQESSRKNKEALA VKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVVY LEEAAQGGQE

[illegible]

FIG. 3
Mouse NRSF Amino Acid Sequence

MATQVMQSSGGSLFNNSANMGMALTNMYYDLHELKSKAELAAP
QLIMLANVALTGEASGCCDYL VGEERQMAELMPVGDNHFSEGEGLSEADLKGLE
NMELGSLELSAVEPQPVFEASAAPEIYSANKDPAPETPV AEDKCRSSKAKPFRCKPCQ
YEAEESEQFVHHIRIHSACKFFVEESAEEKQAKAWESGSSPAEEGEFSKGPIRCDRCGY
NTNR YDHYMAHLKHHLRAGENERIYKCICTYTTVSEYHWRKHLRNHFPRKVYTCSKC
NYFSDRKNYVQHVRTHTGERTPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKCDQCNY
VASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCDYA
ASKKCNLQYHFKSKHPTCPSKRMDVSKVKLKKTKKREADLLNNAVSEKMMENEQTKTK
GDVSGKKNEKPVKAVGKDAKKEKPGSSVSVQVSTRTRKSAVAETKAAEVKHTDQ
TGNNPEKPKAKKNKRKKDAEAHPSEEPVNEGPTKKKKSECKSKISTNVPKGGGRA
EERPGVKKQSASLKKGTNKTTPKTKTSKGGKGLAPKGMGQTEPSSGALAQVGVSPDPA
LIQAEVTGSSSQTELPSPMDIAKSEPAQMEVSLTGPPPVPEPAQMEPSPAKPPQVEAP
TYPQPPQRPAPPTGPAPPTGPAPPTGLAEMEPSPTPSQKEPPPSMEPPCP
EELPQAEPPMEDCQKELPSPVEPAQIEVAQTAPTQVQEEPPPVSEPPRVKPTKRSSL
RKDRAEKELSLSEMARQEQVLMGVGLVPVRDSKLLKGNKSAQDPPAPPSPKGNSR
EETPKDQEMVSDGEGTIVFPLKKGGEAAGESPALAEKESARVSSSEQNSAMPEGG
ASHSKCQTGSSGLCDVDTEQKTDTPVMKDSAAEPVSPPTPTVDRDAGSPA VVASPPIT
LAENESQEIDEDEGIHSHDGSDDLSDNMSEGSDDSLGHGARTPPEATSKNGKAGLAGK
VTEGEFVCIFCDRSFRKEKDYSKHLNRHLNVNVFLEEAEEQEEQEEEEEQEE

FIG. 5
Rat NRSF Amino Acid Sequence

MATQVMGSSGSLFNNSGNMGMALPNDMYDLHDLASKAELAAP
QLIMLANVALTGEVNGSCDYLVGEERQMAELMPVGDNHFSDSEGLEESAELKGDP
SGLDNMELRSLSVVEPQPVFEASAAPEVYSSNKDPAPEAPVAEDCKNLKAKPFR
KPCQYEAEESEEQFVHHIRVHSAKKFFVEESAEEKQAKARESGASPSEEGEFSGPIRCD
RCGYNTNR YDHYTAHLKHLRAGDNERVYKCICTYTTVSEYHWRKHLRNHPRKVVYT
CSKCN YFSTEKN NYVQHVRTH TGERPYKCELC PYSSQKTHLTRHMRTHS GEKPFKCD
QCNYVASNQHEVTRHARQVHNGPKPLNC PHCDYKTADRSNFKKHVELHVNPRQFNCPV
CDYAA SKKCNLQYHFKSKHPTCPSK TMDVSKVKLKKTKRREADLHRDAAAAA TEQTD
EQA KTKGVDA SARSRERPVKGVGKDV PKEKKPCSNASVVQVTTTRKSAVETKAAEGK
HTDGGTGNNAEKSSKAKSKRKMDAEAHPSVEPVTEGPVTKKKKTESKPKTSGEVPKG
SRVEDRKADKQQSASIKKGGKKTALKTKAKGSKLAPKWVGHTEPSSEMAQGGE
SPV
PALTQAVVTPSGSTQTELS SPMEDIAQTEPAQMDVSQTGPPQVQRPLPVEPAQLEPSPP
QEPPQVEPPACVEPPPPVEPPCPMEPAEMEPPMPESQVEPPPHLEPPLPMELPQVE
LPPVEDCQKELPPVEHAQTKVAQTGPTQVGAVQEEPLFCLRATSSQANQKVISPKDRA
KEKLSVLSEMARQEQVLEVGLVPVRDSQLLKASKSAPDLPAPPSPLPKGHLRREETP
KDQEMFSDGEGNKVSPLEKGGTEEAGESRAELAAPMESTSALSSESSNAPDGETLHS
ECQADSTAVCEMEVDTEQKTD RVP LKDSAVEPV SPLNPRVDPEAAAPAVVASPPITLA
ESQEIDEDEGIHSHDGS DLSDNMSEGSDDSLGHGARPAPQEA TSKSGKEGLAVKVTEG
EFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEAAEEQ

FIG. 6

Rat NRSF cDNA Sequence

atgagccacc aggtgatgagg gcagcttctt ggaaggaggaa gtcctttaa caacagtgcc 61 aacatgggca tggccttacc caacgacatg tatgacttgc acgaccttgc gaaagctgaa 121
ctggcggcac ctacgctcat tatgttagcc aacgtggccc tgaactgggga agtgaatggc 181 agctgctgig attacctgtg tgggtgaagag agacagatg cctggttgat gctgttgga
241 gacaacct tttagatag cgaagagaa ggccttgagg agctggctga actaaaggt 301 gaccccaagtg ggcctgggaca catgggaacg agaaagttgg agctaaagcgt
tgaagagccc 361 cagcccgat ttgaagcatic agctggccca gaagtgatca gtcgaatga agatccgcc 421 cctgaagcac cctgggcgga ggaacaatgc aagaattga
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ctgcacgtca accctggca gttcaactgc cctgtgtgtg actacgggccc ctcaagaag 1201 gtttaacctgc agttaccaag caccacct gcccacagca gacgatggac
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2821 gactcagcag tagaaccagt gtcacttt aacccagag tggaccctga agcagcgagg 2881 cagctgtgag gggggaggt 3001 gactcagagc tgcattggggc tggggcagc ccaacaggag
tgatgagat 2941 gaaggcatic acagccatga tggaaagtac ctgagcgaca acatgtctga gggggaggt 3061 gaaagggttgg cgttcaagt aactgtggga gagttgtt gtagctgt 3121 ttgaaagag aaaaagacta tagcaaacac ctcaatggcc
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attgtgttaa tgtgtattc 3181 cttgaagaaag cagctgagga gcaaggagtag agtagctgat cctcgaaggag aagcgcaatg 3241 cgaattgtg a

FIG. 7
Xenopus NRSF partial Amino Acid Sequence

MATQMVNQSTGNSLFCSTSTYSNISLDNDMYGLHDLKADMAAPR
LIMLANVALTGELSSGCCDYTPGERQMAELTTVNDNSFSDSEGRLEDSPSMDIQSH
NFIMEMEPAECSKEGTSENDGTLISNTLEVEVQKDKRTPSPTDDKYKCVKSKPFRCKP
CQYKAEESEEFVHHIKHS AKIYVDNDSNKKAAQNEADSSISESDVSKGPIQCDCRG
YNTNRFDHYL A HLKHHNKAGENERVYKCTICTYTTVSEYHWKKHLRNHYPRILYTCSQ
CSYFSDRKNNYIQHIRTHTGERPYQCILCPYSSSQKTHLTRHMRTHSGEKPFKCEQCS
YVASNQHEVTRHARQVHNGPKPLTCPHCDYKTA DRSNFKKHVELHVNPRQFLCPVCDY
AASKKCNLQYHIKSRHSGCTNITMDVSKVKLRTKKGDIGVADV DANKQTENGNIIDKS
VEETVKA EKRESCGKAKKSIVNLVDGQVAKRRRLSSTQKKIKTSDARPEKILDKSRKS
SCVKKRKS DLENSNDTQTSTV

FIG. 8
Xenopus NRSF partial cDNA sequence

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1  ggcacgagca gtcggttgag acgcgattt  gagaacgtg  gacagttctt gaatttggga
61  gggagaatgg cgcaagtgtg cgacgggatt ccgaaaagt tataaacatg gccactcaaa
121  tggtaacca gtctacaggt aacagcttgt tctgtaccag cacctactcc aatatttcat
181  tggacaatga catgtatggg ttgcattgac ttcaaaagc tgatatggca gccctcgat
241  tgataatgct agcaaatgtg gctctgactg gcgaactcag tagtggttgc tgtgattaca
301  cgccagaagg agaaaggcaa atggcagaac taacaactgt aaatgacaac agcttctcag
361  atagtggagg gatataggtg gaagattcac ccagcatgga tattcagtc cacaatttta
421  taatggagat ggagccagct gaatgttcaa aagaaggaa gtctgaaaat gatggaactc
481  tactctctaa tacacttgag gtggaggttc aaaaggataa agggacaccc agcccaacag
541  atgacaaaata caaatgtgtg aaagcaaac catttcgtg caaaccttgt cagtacaaag
601  cagagtctga agaagaattt gtcatcaca ttaagattca cagcgtaag atatatgtg
661  ataatgactc aaataaaaaa ggcagggtta atgaggcaga ttctagcata tcggaggaaat
721  ctgatgtctc caaaggacct attcagtggtg acaggtgtgg atacaataca aatcgttttg
781  atcactatct ggctcattta aagcatcaca acaaaagtgg agaaaatgaa agagtataca
841  aatgtacaat atgtacttat actacagtca gtgaatatca ctggaagaaa catctacgta
901  accattatcc aaggatactc tatacatgct cacaatgttc ctatttttct gataggaaaa
961  ataattatat ccagcatata agaacacata caggagaacg accatatcag tgtattctat
1021  gtccttactc aagctcacag aaaaccact tgaccaggca catcgaaact cattcagggtg
1081  agaagccttt caaatgtgag cagtgtagtt atgttgcatc caatcagcat gaagttacac
1141  gtcatgcaag acaggttcac aatggaccac aaccattaac ttgccctcat tgtgactaca
1201  aaactgcaga tcgcagtaat ttcaagaagc atgtagagtt acatgttaat cctcgacagt
1261  ttctatgccc tgtttgtgac tatgtgctt ccaaaaagtg taacttgcaa tatcatataa
1321  aatccagaca ctcaggatgc acaaatatca caatggatgt ttccaaagta aaactgagga
1381  caaagaaaagg agacatagga gttgcagatg ttgatcaaaa taagcaaaaa gagaatggaa
1441  atataataga taaatctgtg gaagagaccg ttaagcaga gaaaagggaa agctgtggga
1501  aagctaaaaa aagtattgtt aatttagttg atggccaggt tgcaaaaaaa aggcgcttgt
1561  catctactca gaaaaaatt aaaacttcag acgcaaggcc tgaaaagatt ttagataaat
1621  cccgtaagtc tagttgtgtg aaaagaaaat ctgatttatt agaaaattct aatgatcccc
1681  aaacaagcac tgtg

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FIG. 9



Zif268 RPYA CPVES CDRRFS RSDELTR HIRI - HTGQK P
 FQCRI -- CMRNFS RSDHLTT HIRT - HTGEK P
 FACDI -- CGRKFA RSDEKRR HTKI - HLRQKD

NRSF KPFR CKP -- CQYEAEE SEEQFVH HIRV - HSAKKFFVEESAEEKQAKARESGSSSTAEEGDFSKGP
 IR CDR -- CGYNTN RYDHYTA HLKH - HTRAGDNERV
 YK CII -- CTYTTV SEYHWRK HLRN - HFPRKV
 YTCGK -- CNYFSD RKNNVVQ HVRT - HTGERP
 YK CEL -- CPYSSS QKTHLTR HMRT - HSGEKP
 FK CDQ -- CSYVAS NQHEVTR HARQV HNGPKP
 LN CPH -- CDYKTA DRSNFCK HVEL - HVNPRQ
 FN CPV -- CDYAAS KKCNLQY HFKSK HPTCPN

FIG. 10

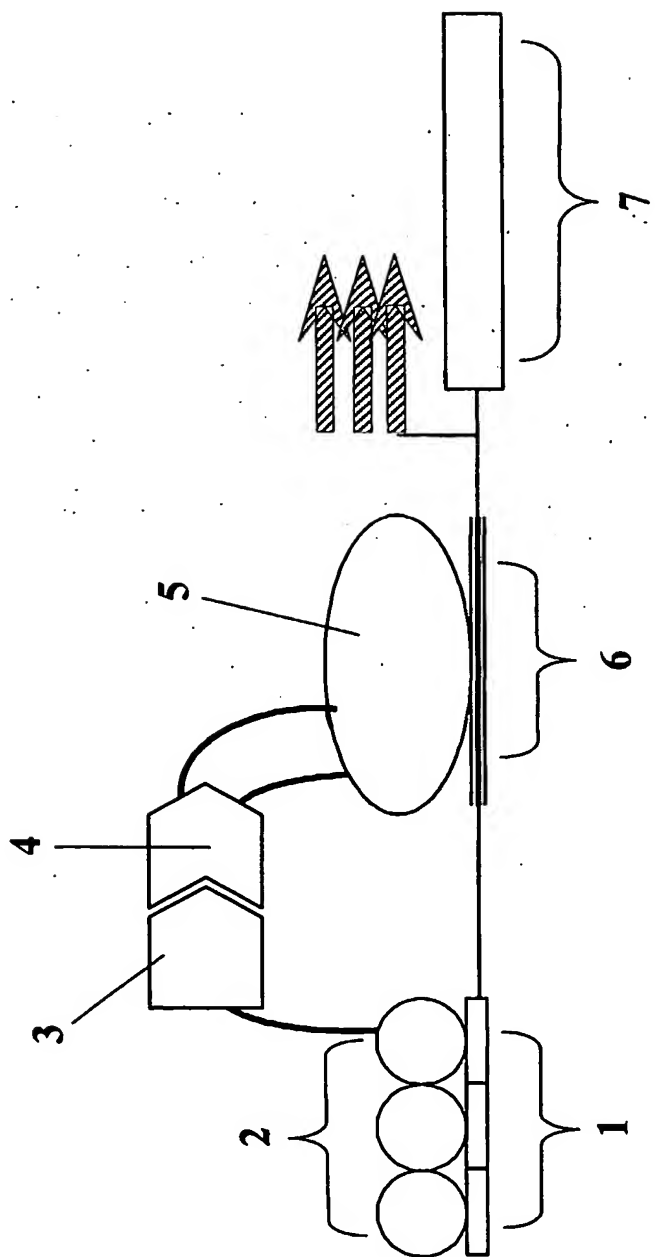


FIG. 11

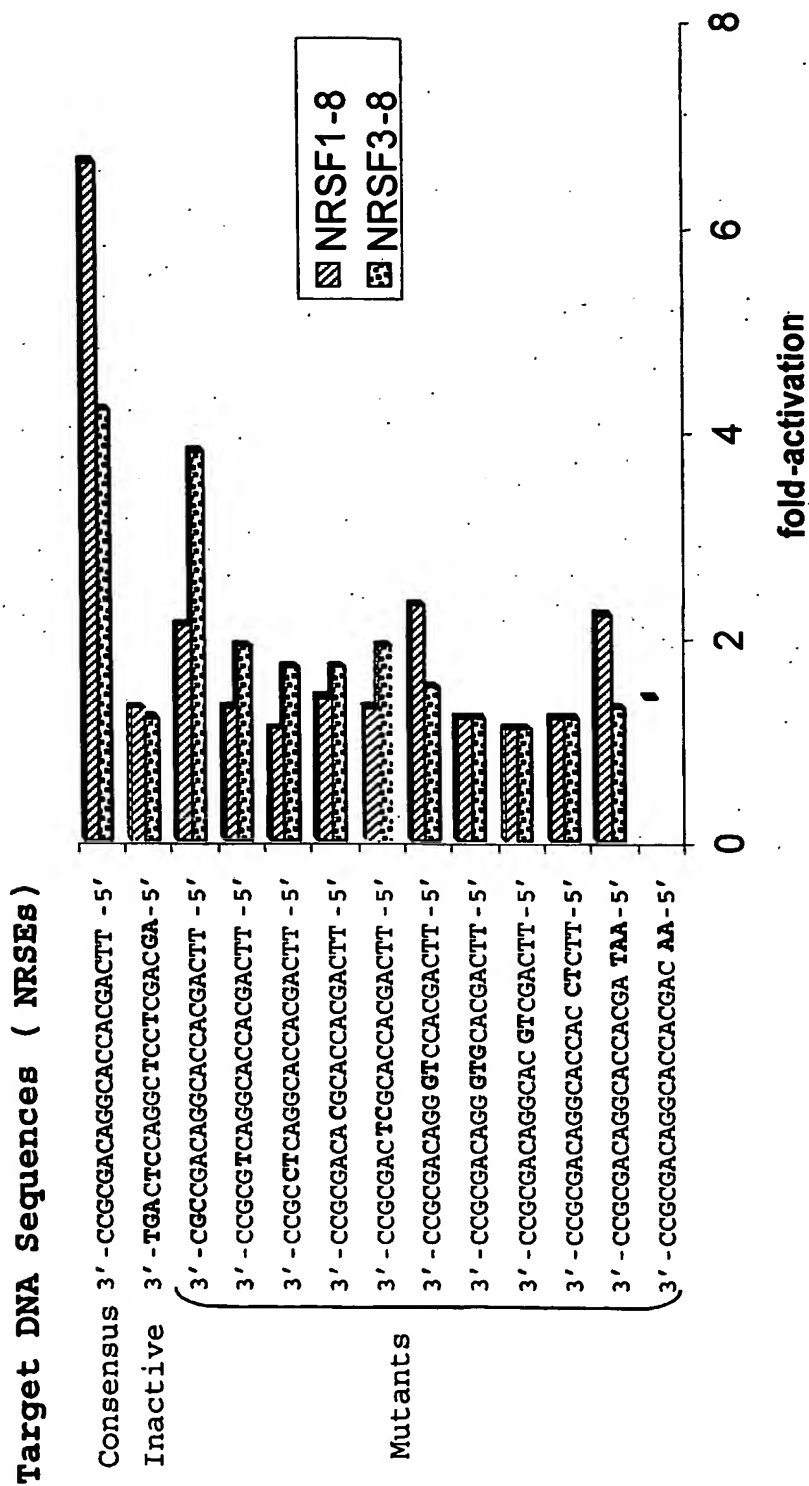


FIG. 13

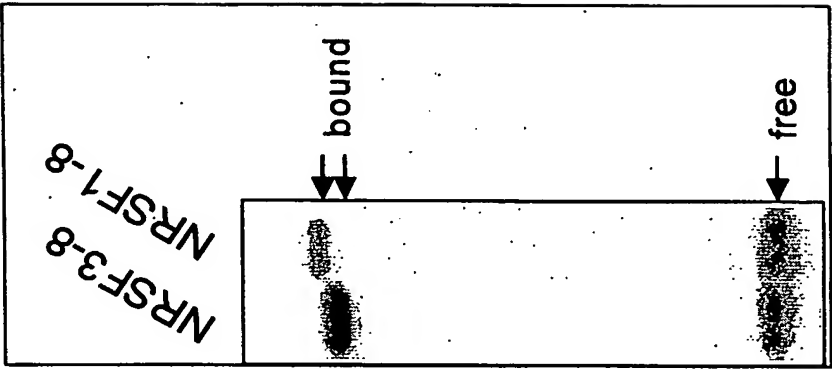


FIG. 14

A. Finger 4 Selections		B. Finger 5 Selections	
3'-CCGGCCTCAGGCACGACTT-5'		3'-CCGGGACTCGCACCACGACTT-5'	
-1	1 2 3 5 6	-1	1 2 3 5 6
NRSF F4v1	H K T R M E	NRSF F5v1	T V G T R R
NRSF F4v2	H K T R M E	NRSF F5v2	T R G T K R
NRSF F4v3	H K T R M E	NRSF F5v3	T G S T R R
➔ NRSF F4v4	H R T R M E	➔ NRSF F5v4	T M S G R R
NRSF F4v5	H K T R K E	NRSF F5v5	T I S A R R
NRSF F4v6	H L T R K E	➔ NRSF F5v6	H M P T R R
NRSF F4v7	H K T R A E	NRSF F5v7	H R G T V R
➔ NRSF F4v8	H K T R D E	NRSF F5v8	R A P D K R

FIG. 15A

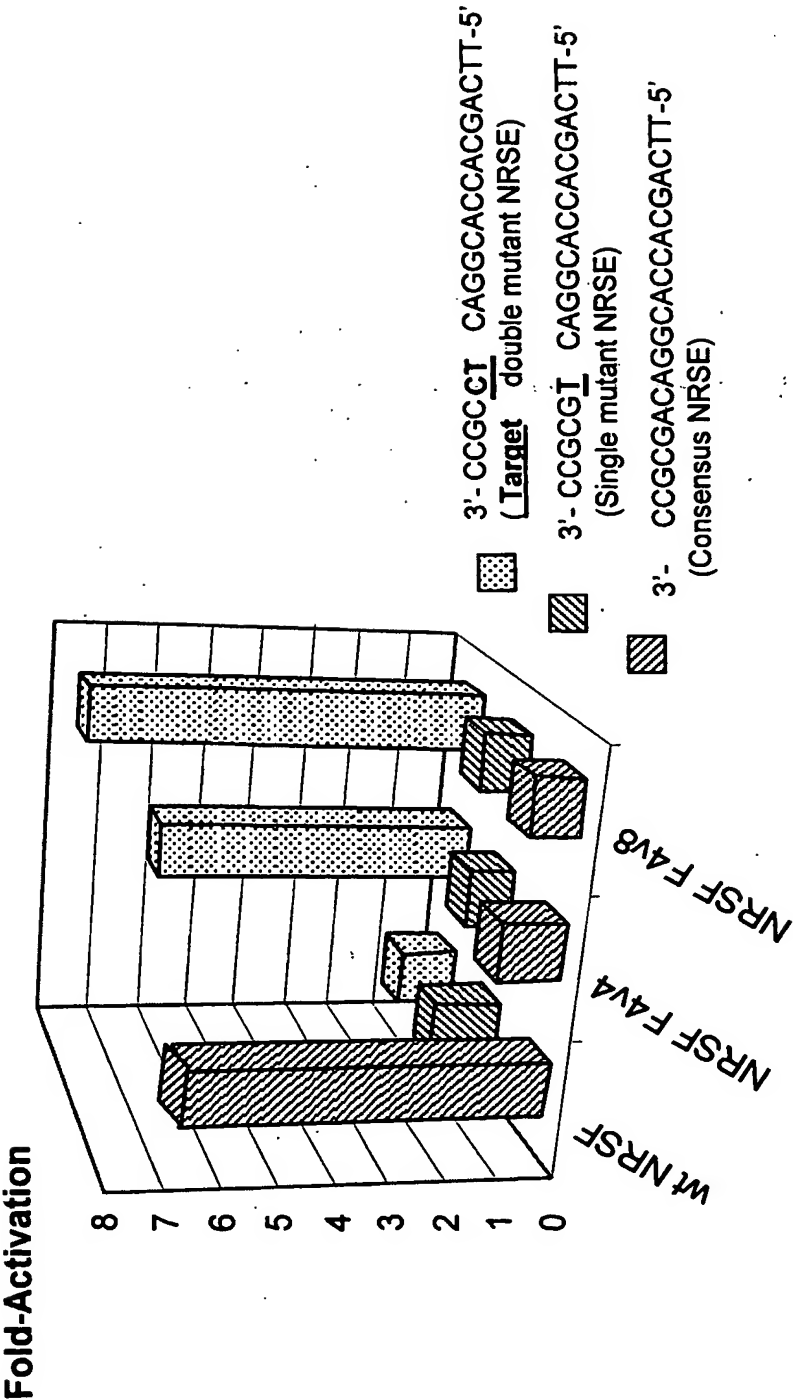


FIG. 15B

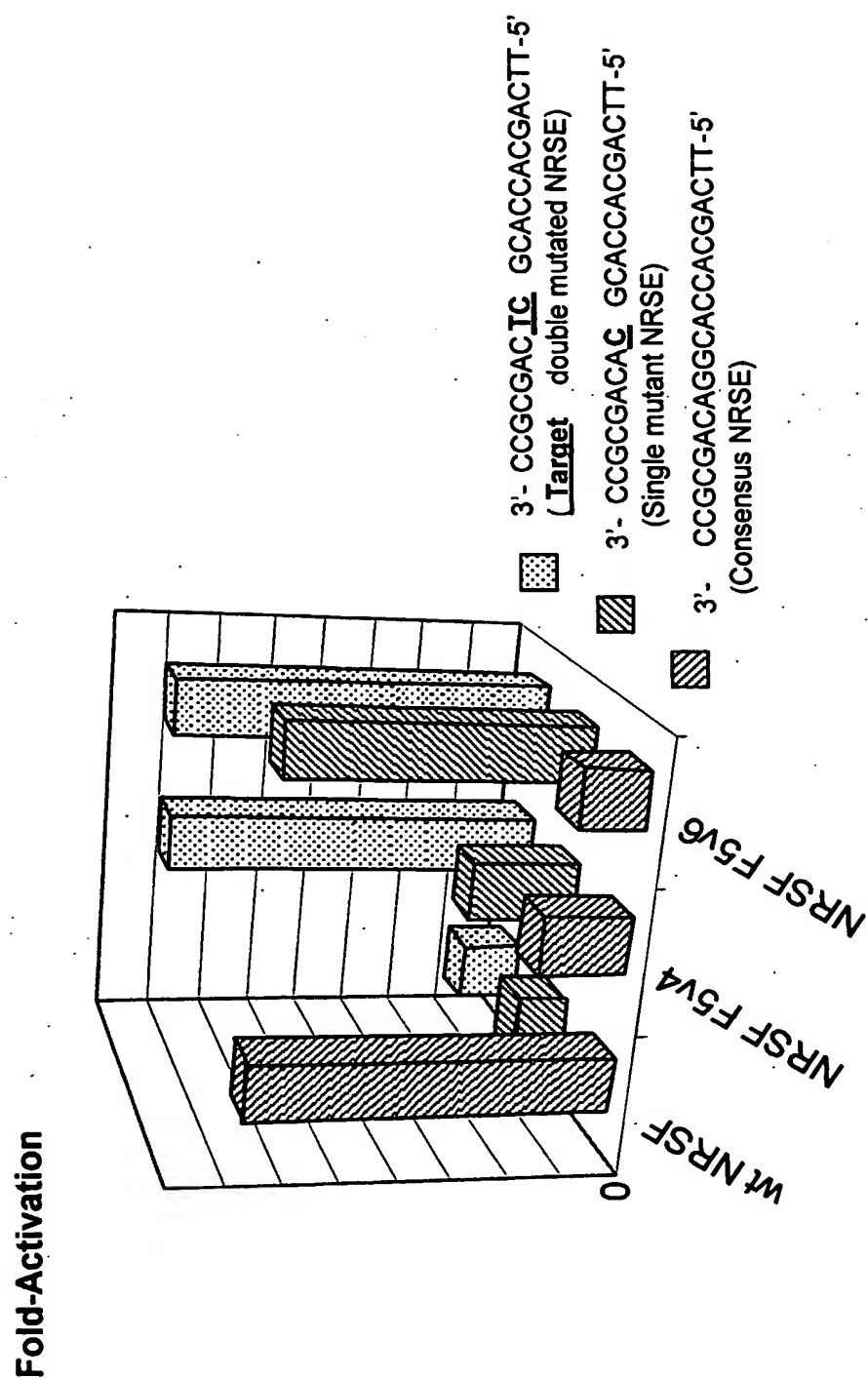


FIG. 16

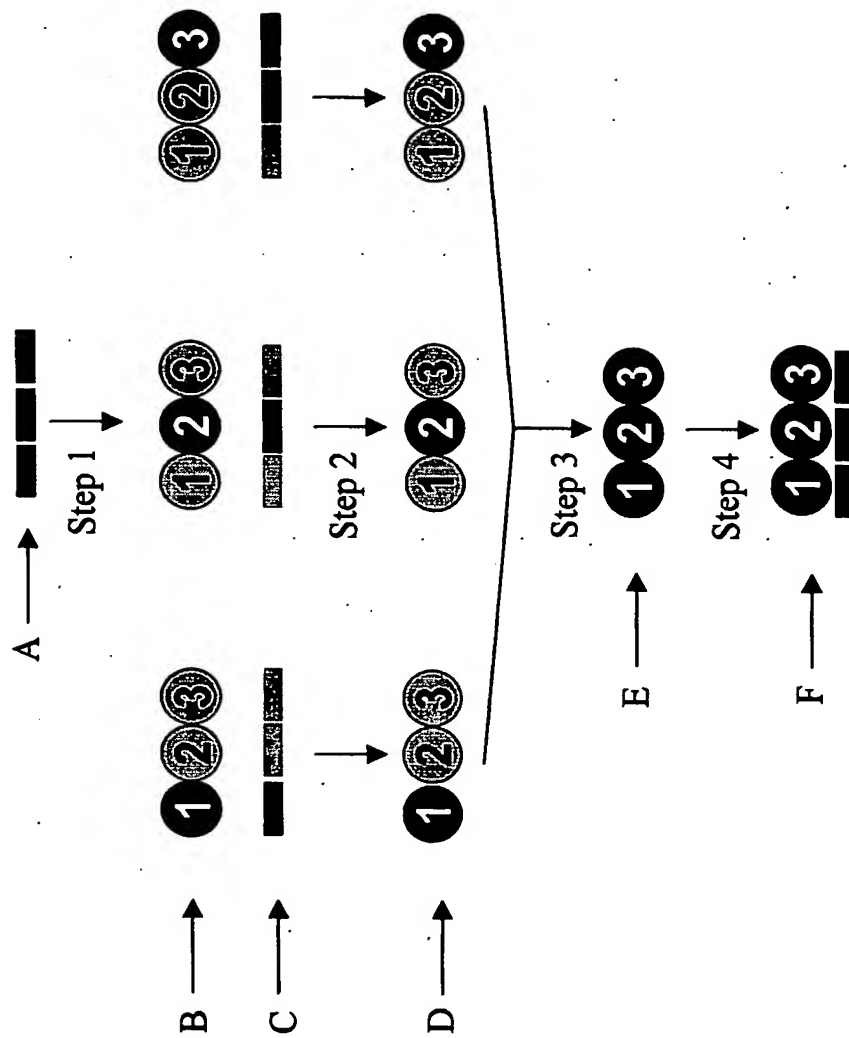


FIG. 17

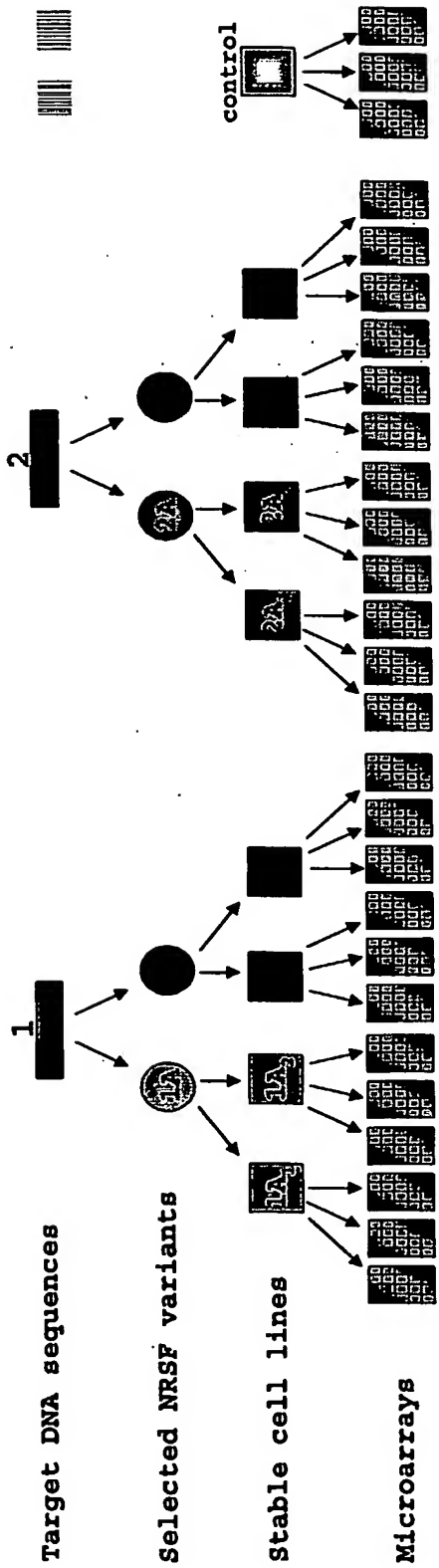


FIG. 18

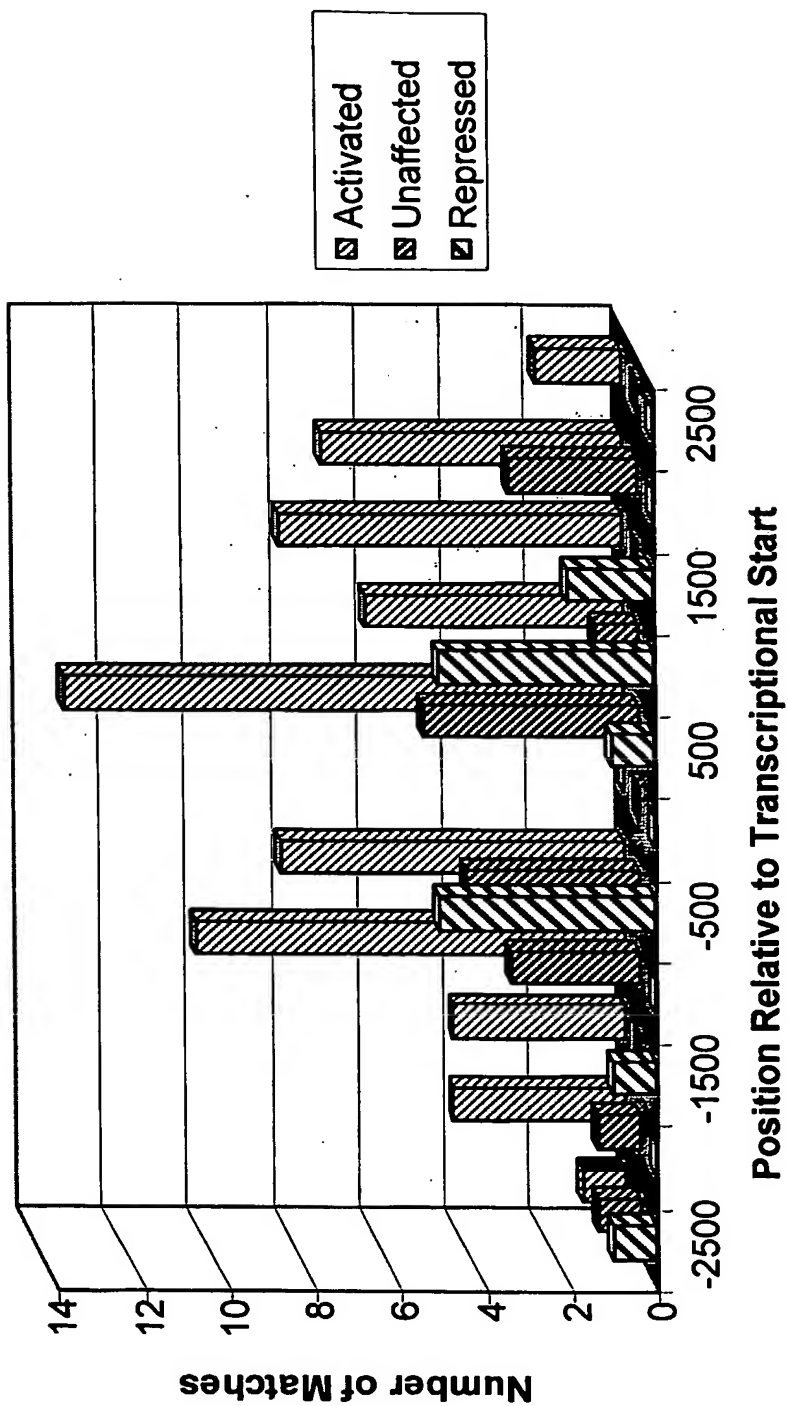


FIG. 19**F4v1 (sequence identical to F4v2, F4v3)**

MATQVMGQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLLSVVEPQPVFEEASGAPDIYSSNKDLPPEPTPGAEDKGKSSKTKPFR
CKPCQYEAESSEEQFVHHIRVHSAKKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYSFSDHKTRYMEHVTRHTGERPYKCELCPYSSSQKTHLT
RHMRTSHGKPKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDSVKVCLKTKKKREADLPDNI TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKPKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSSHGHGPNDEESTTKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPPAPTEAVQKGPVQVELPPMEHAQME
GAQIRPAPDEPVQMEVVEGPAQKELLLPPVEPAQMVGAQIVLAHMLPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPMEVVQKEPVQKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLEI VGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSGQNLNTPEGETLNGKHQTD SI VCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGGQ

FIG. 20

F4V4

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG
DNNFSDSEEGGLEESADIKGEPHGLENNMELRSL ELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESSEEQFVHHIRVHSAKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCN YFSDHRTRYMEHV RTHTGERPYKCELCPYSSSQKTHLT
RHMRTSHGKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVD SHSLHGPVNDEESSSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME
GAQIRPAPDEPVQMEVVEVQEGPAQKELLPPVEPAQMVGAQI VLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMVEVVQKEPVQIELSPPMVEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPLRKDKKEKSNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINETHISSGQNLNTPEGETLNGKHQTD SIVCEMKMTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAAQGGQE

FIG. 21

F4v5

MATQVMGSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGELEESADIKGEPHGLENNMELRSLSELSVPEPQVFEEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESAEEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNVFSDFHKTTRYKEHVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTSHGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAAASK
KCNLQYHFKSKHPTCPNKTMDSKVKLKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKL EVD SHSLHGPVNDEESTK KKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVQKEPVQIELSPMEVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESTHIS SSGQNLTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGD FVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEA AQQE

FIG. 22

F4v6

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGGLEESADIKGEPHGLENMELRSLSVPEPQVFEEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPKVVYTCGKCNYSFSDHLTRYKEHVTRHTGERPYKCELCPYSSSQKTHLT
RHMRTSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLLKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSSH LGPVDNEESSTKKKKVESKSKNNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVVELPPPMHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMELSPPMVQKEPVQKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESTHIS SSGQNLTPEGETLINGKHQTD SIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAAQQQE

FIG. 23

F4v7

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENNMELRLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR
CKPCQYEAESSEEQFVHHIRVHSAKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCN YFSDHKTRYAEHVTRHTGERPYKCELCPYSSSQKTHLT
RHMRTSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVDYAAASK
KCNLQYHFKSKHPTCPNKTM DVSKVKLLKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVD SHSLHGPVNDEESSTKKKKVSKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPMEVVQKEPVQKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KLNTGEGNKEAPLQKVGAEEADESLPGLAANIN ESTHISSSGQNLNTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAQQQE

FIG. 24

F4v8

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAE LAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLLELSVVEPQPVFEASGAPDIYSSNKDLPPEPTPGAEDKGSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYSDHKTRYDEHVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTSHGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDSVKVLLKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVD SHSLHGPVNDDEESSTK KKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMHQAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT
GINSTVEEPPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEA AQQE

FIG. 25

F5V1

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGGLEESADIKGEPHGLENNMELRSLSELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCNFYFSDRKNNYVQHVTRHTGERPYKCELCPYSSSTVGTLR
RHMRTSGEKPFPKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVC DYAAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSSHLPVNDDEESTTKKKKVESKSKNNSQEVPK
GDSKVEENKQNTCMKKSTKKKTLKNKSSKKSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAQQQE

FIG. 26

F5v2

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENNMELRSLLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESSEEQFVHHIRVHSAKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYFSDRKNNYVQHVTRHTGERPYKCELCPIYSSSTRGTLK
RHMRTSHGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKKNESVKA EKRDVSKKPKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKL EVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKS TKKKTLKNKSSKKSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLRREEASGDQ
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINETHISSSGQNLNTPEGETLNGKHQTD SI VCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQ EIDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLNVVYYLEEAAQGGQ E

FIG. 27

F5V3

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGELEESADIKGEPHGLENMELRSLSVVEPQPVFEASGAPDIYSSNKDLPPEPTGAEDKGKSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYFSDRKNNVVQHVRTHTGERPYKCELCPYSSSTGSTLR
RHMRTSHGEKPFKCDQCYSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTAADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLLKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLVDSSHSLHGPVNDSEESTKTKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELEPPMETAQTEVAQMGPPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMELSPMEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPLLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KLNTGEGNKEAPLQKVGAEAEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAQQQE

FIG. 28

F5v4

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGGLEESADIKGEPHGLENMELRSLSELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAEESEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCNFYFSDRKNNVYQHVRTHTGERPYKCELCPYSSSTMSGLR
RHMRTSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTA DRSNFKKHVELHVNPRQFNCPCVCDYAAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNI TNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKL EVDSHSLHGPVNDEESSTKKKKVSKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKESNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHIS SSGQNLNTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEAQQQE

FIG. 29

F5v5

MATQVMQSSGGGLFTSSGNIGMALPNDWYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGGLEESADIKGEPHGLENMELRSLLELVVEPQPVFEASGAPDIYSSNKDLPPEPTPGAEDKGKSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSTISALR
RHMRTSHSGEKFCKDCQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLVDSSHSLHGPVNDDEESSTKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGSQAQMDPPQMGPAPEAVQKGPVQVELPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELEPPMETAQTEVAQMGPAPEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPLLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEAEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTD SI VCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVVYLEEAAQGOE

FIG. 30

F5v6

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDL SKAE LAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGGLEESADIKGEPHGLENMELRSL ELSVVEPQPVFEASGAPDIYSSNKDLP PETPGAEDKGKSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAK KFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCN YFSDRKNNVYQHVRTHTGERPYKCELCPYSSSHMPTLR
RHMRTSHSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTM DVSKVKLKKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKR KLEVDSSH LGPVNDEESSTK KKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGS AQMDPQMGPA TEAVQKGPVQVELPPPMHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMELSPMEVVQKEPVQIELSPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPLLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KL LNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQ TDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEA AQQE

FIG. 31

F5v7

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAE LAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGELEESADIKGEPHGLENMELRSLLELSVVEPQPVFEASGAPDIYSSNKDLPPEPTPGAEDKGSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYFSDRKNNYVQHVTRHTGERPYKCELCPYSSSSHRGTLV
RHMRTSHSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDSVKVCLKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHLHGPVNDEESSTKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPPMETAQTEVAQMGPPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPLLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTD SI VCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEAAGQE

FIG. 32

F5v8

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENNMELRSLSELSVVEPQPVFEEASGAPDIYSSNKDLPETPGAEDKGKSSKTKPFR
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDCGYN TNRYDHYTAHLKHHTR
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCN YFSDRKNNYVQHVRTHTGERPYKCELC PYSSSRAPDLK
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLLKTKKKREADLPDNI TNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKKPS
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKSKRKL EVDSHLGPVNDEESSTKKKKKVESKSKNNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPMEHAQME
GAQIRPAPDEPVQMEVQEGPAQKELLPPVEPAQMVGAQIVLAH MELPPPME TAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVQKEPVQIELSPMEVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHIS SSGQNLTPEGETLNGKHQTD SI VCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQ EIDEDEGIHSEGS DLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHL VNVYYLEEAAQGGQ

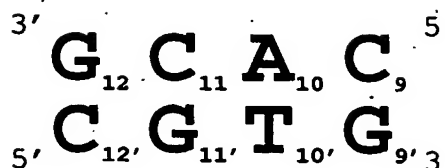
FIG. 33

A.

wild-type F6

-112356

NQHETR

relevant portion
of NRSE

B.

F6 variants/
base 9

-112356

DRGNRR

DRGNNR

DKANAR

DLSNRR

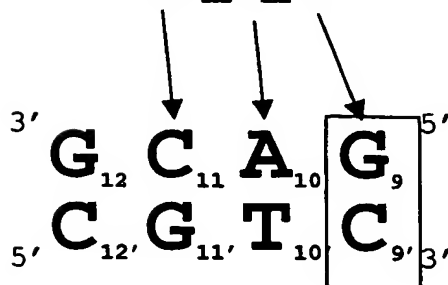
DSTNKR

ERGNQR

ERYAVR

EKYKVI

D+ _N_ R

F6 variants/
base 11

-112356

RREREL

RREKVM

RRERYI

RRDNET

RRDGAN

RKDLAL

RADIRL

RLELVK

RRD _

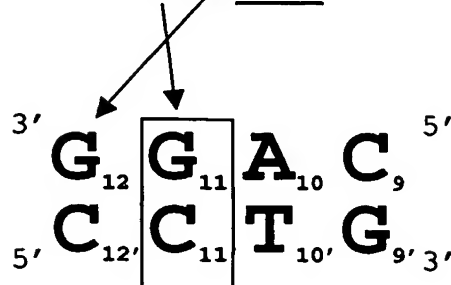
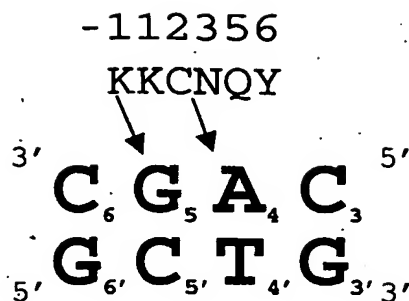


FIG. 34

A.

wild-type F8

relevant portion
of NRSE

B.

F8 variants/
base 3

-112356

RLFNRR

KKYNRR

RQYNQR

TKFNHR

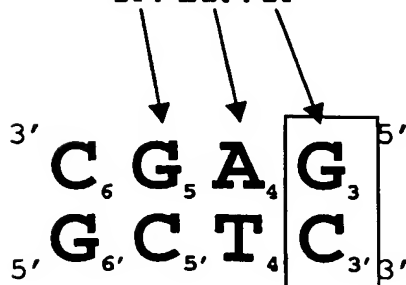
RKYNRR

RKYNRR

RRANVR

RFYNRR

R+YN+R

F8 variants/
base 4

-112356

RRSTRY

RRSTRY*

RRSTRY*

RKATDY

RRTTLY

RKATMY

RRSTQY

RRSTVY

R+sT_Y

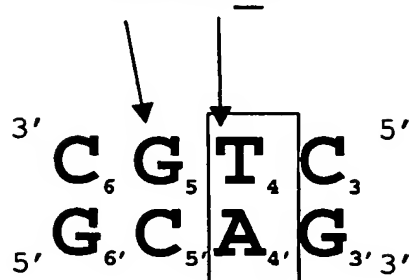


FIG. 35

